SEQUENCE LISTING

| <110> DAI, KEN-SHWO | | | | | | | | | | | | | | |
|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|
| <120> HUMAN SACH-RELATED GENE VARIANTS ASSOCIATED WITH CANCERS | | | | | | | | | | | | | | |
| <130> U 014797-5 | | | | | | | | | | | | | | |
| 10/653,680 2003-09-02 | | | | | | | | | | | | | | |
| <160> 6 | | | | | | | | | | | | | | |
| <170> PatentIn version 3.2 | | | | | | | | | | | | | | |
| 10> 1 11> 1960 12> DNA 13> ARTIFICIAL SEQUENCE | | | | | | | | | | | | | | |
| <220> <223> A Variant of a human SACH gene | | | | | | | | | | | | | | |
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| ggcgagtgaa agaaggaaat cagaaaggaa gggagttaac aaaataataa aaacagcctg 120 | | | | | | | | | | | | | | |
| agccacggct ggagagaccg agacccggcg caagagagcg cagccttagt aggagaggaa 180 | | | | | | | | | | | | | | |
| cgcgagacgc ggcagcgcag agcgcgcagc agcagcagca gcagcagcag cagcagcagc 240 | | | | | | | | | | | | | | |
| aggcgccgca gctgagaccg gcggccgacg gccagccctc agggggcggt cacaagtcag 300 | | | | | | | | | | | | | | |
| cgcccaagca agtcaagcga cagcgctcgt cttcgcccga actg atg cgc tgc aaa 356 Met Arg Cys Lys 1 | | | | | | | | | | | | | | |
| cgc cgg ctc aac ttc agc ggc ttt ggc tac agc ctg ccg cag cag cag Arg Arg Leu Asn Phe Ser Gly Phe Gly Tyr Ser Leu Pro Gln Gln 5 10 15 20 | | | | | | | | | | | | | | |
| ccg gcc gcc gtg gcg cgc cgc aac gag cgc gag cgc aac cgc gtc aag Pro Ala Ala Val Ala Arg Arg Asn Glu Arg Glu Arg Asn Arg Val Lys 25 30 35 | | | | | | | | | | | | | | |
| ttg gtc aac ctg ggc ttt gcc acc ctt cgg gag cac gtc ccc aac ggc 500 Leu Val Asn Leu Gly Phe Ala Thr Leu Arg Glu His Val Pro Asn Gly 40 45 50 | | | | | | | | | | | | | | |
| gcg gcc aac aag aag atg agt aag gtg gag aca ctg cgc tcg gcg gtc 548 Ala Ala Asn Lys Lys Met Ser Lys Val Glu Thr Leu Arg Ser Ala Val 55 60 65 | | | | | | | | | | | | | | |

| | | | cgc Arg | | | | | | | | | | | | | į | 596 |
|------|-------|-------|-------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|------|-----|
| | | | ttc Phe | | | | | | | | | | | | | ŧ | 644 |
| | | | gac Asp | | | | | | | | | | | | | • | 692 |
| | | | gag Glu 120 | | | | | | | | | | | | | | 740 |
| | | | ttc Phe | | | | ttct | gagg | aaa (| ctcgg | geetg | gg to | cagg | cccts | 3 | • | 791 |
| gtgo | cgaat | gg | acttt | ggaa | ag ç | agggt | tgato | gca | acaa | cctg | cato | cttta | agt | gctt | cttg | t f | 851 |
| cagt | ggcg | jtt (| gggag | 3999 | ga ga | aaaa | ggaaa | a aga | aaaa | aaaa | agaa | agaag | gaa | gaaga | aaaag | a ! | 911 |
| gaag | gaaga | aaa a | aaaac | gaaa | aa ca | agtca | aacca | aco | cccat | cgc | caac | ctaag | gcg | aggca | atgcc | t ! | 971 |
| gaga | agaca | atg 9 | gcttt | caga | aa aa | acggg | gaago | gct | caga | aaca | gtat | cttt | gc . | actco | caatc | a 10 | 031 |
| ttca | acgga | iga i | tatga | aaga | gc aa | actg | ggaco | tga | agtca | aatg | cgca | aaaat | tgc . | agcti | gtgt | g 10 | 091 |
| caaa | agca | ıgt (| gggct | cct | gg ca | agaag | gggag | g cag | gcaca | acgc | gtta | atagt | caa | ctcc | catca | c 1 | 151 |
| ctct | aaca | ecg (| cacag | gctga | aa ag | gttct | ttgct | cgg | ggtco | cctt | caco | ctcc | ccg | ccctt | tctt | a 12 | 211 |
| gagt | gcag | gtt (| cttag | gccct | c ta | agaaa | acgaç | g ttg | ggtgt | ctt | tcgt | ctca | agt . | agcc | ccac | c 12 | 271 |
| ccaa | ataag | gct (| gtaga | acati | g gt | tttad | cagto | g aaa | actat | gct | atto | ctcag | gcc | cttt | gaaac | t 13 | 331 |
| ctgo | ettet | cc | tccag | gggc | cc ga | attco | ccaaa | cc | ccat | ggct | tcc | ctcad | cac | tgtct | tttc | t 13 | 391 |
| acca | attt | ca | ttata | agaat | g c | ttcca | aatct | ttt | gtga | aatt | tttt | atta | ata | aaaa | atcta | t 14 | 451 |
| ttgt | atct | at | cctaa | acca | gt to | gggg | gatat | att | aaga | atat | tttt | gtad | cat | aaga | gagaa | a 15 | 511 |
| gaga | agaga | aaa a | aattt | tata | ga ag | gttt | tgtad | aaa | atggt | tta | aaat | gtgt | tat | atcti | tgata | c 15 | 571 |
| ttta | acat | gt | aatgo | ctati | a co | ctct | gcata | ttt | taga | atgt | gtag | gttca | acc | ttaca | aactg | c 16 | 631 |
| aatt | ttc | ct a | atgto | ggtti | t g | taaag | gaact | cto | cctca | atag | gtga | agato | caa | gaggo | ccacc | a 16 | 691 |
| gtto | gtact | tc | agcad | ccaat | g to | gtctt | tactt | tat | agaa | aatg | ttgt | taat | tgt | attaa | atgat | g 1 | 751 |
| ttat | taaa | ata (| ctgtt | caa | ga a | gaaca | aaagt | tta | atgca | agct | acto | gtcca | aaa | ctcaa | aagtg | g 18 | 811 |
| cago | ccagt | tg | gtttt | gata | ag gi | ttgc | ctttt | gga | agatt | tct | atta | actgo | cct | tttti | ttct | t 18 | 871 |
| acto | gttt | at | tacaa | aacti | ca ca | aaaa | atato | j tat | caaco | cctg | tttt | atac | caa | actag | gtttc | g 19 | 931 |
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- <213> ARTIFICIAL SEQUENCE

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<223> A peptide encoded by a variant of a human SACH gene

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Pro Gln Gln Gln Pro Ala Ala Val Ala Arg Arg Asn Glu Arg Glu Arg 20 25 30

Asn Arg Val Lys Leu Val Asn Leu Gly Phe Ala Thr Leu Arg Glu His 35 40 45

Val Pro Asn Gly Ala Ala Asn Lys Lys Met Ser Lys Val Glu Thr Leu 50 55 60

Arg Ser Ala Val Glu Tyr Ile Arg Ala Leu Gln Gln Leu Leu Asp Glu 65 70 75 80

His Asp Ala Val Ser Ala Ala Phe Gln Ala Gly Val Leu Ser Pro Thr 85 90 95

Ile Ser Pro Asn Tyr Ser Asn Asp Leu Asn Ser Met Ala Gly Ser Pro
100 105 110

Val Ser Ser Tyr Ser Ser Asp Glu Gly Ser Tyr Asp Pro Leu Ser Pro 115 120 125

Glu Glu Glu Leu Leu Asp Phe Thr Asn Trp
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- <210> 3
- <211> 1994
- <212> DNA
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Met Ser Lys Val Glu Thr Leu Arg Ser Ala Val Glu Tyr Ile Arg Ala 1 5 10 15

Leu Gln Gln Leu Leu Asp Glu His Asp Ala Val Ser Ala Ala Phe Gln 20 25 30

Ala Gly Val Leu Ser Pro Thr Ile Ser Pro Asn Tyr Ser Asn Asp Leu 35 40 45

Asn Ser Met Ala Gly Ser Pro Val Ser Ser Tyr Ser Ser Asp Glu Gly 50 55 60

Ser Tyr Asp Pro Leu Ser Pro Glu Glu Glu Leu Leu Asp Phe Thr 65 70 75 80

Asn Trp

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      (569) . . (805)
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                                                                  120
agccacggct ggagagaccg agacccggcg caagagagcg cagccttagt aggagaggaa
                                                                  180
cgcgagacgc ggcagagcgc gttcagcact gacttttgct gctgcttctg cttttttttt
                                                                  240
tettagaaac aagaaggege cageggeage etcacaegeg agegeeaege gaggeteeeg
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aagccaaccc gcgaagggag gaggggaggg aggaggaggc ggcgtgcagg gaggagaaaa
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                                                                  480
cccaagttct ctctgtgtcc ccctcgcggg ccccgcacct cgcgtcccgg atcgctctga
                                                                  540
ttccgcgact ccttggccgc cgctgcgc atg gaa agc tct gcc aag atg gag
                                                                  592
                             Met Glu Ser Ser Ala Lys Met Glu
                              1
age gge gge gge cag cag cec cag ceg cag cec cag cag cec tte
                                                                  640
Ser Gly Gly Ala Gly Gln Gln Pro Gln Pro Gln Pro Gln Pro Phe
   10
ctg ccg ccc gca gcc tgt ttc ttt gcc acg gcc gca gcc gcg gcg gcc
                                                                  688
Leu Pro Pro Ala Ala Cys Phe Phe Ala Thr Ala Ala Ala Ala Ala Ala
25
                   30
736
Ala Ala Ala Ala Ala Ala Gln Ser Ala Gln Gln Gln Gln Gln Gln
                                                                  784
cag cag cag cag cag gcg ccg cag ctg aga ccg gcg gcc gac ggc
Gln Gln Gln Gln Gln Ala Pro Gln Leu Arg Pro Ala Ala Asp Gly
           60
cag ccc tca ggg ggc ggt cac aagtcagcgc ccaagcaagt caagcgacag
                                                                   835
Gln Pro Ser Gly Gly His
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cgctcgtctt cgcccgaact gatgcgctgc aaacgccggc tcaacttcag cggctttggc 895 955 tacagcetge egeageagea getgetggae gageatgaeg eggtgagege egeetteeag 1015 graggegtee tgtegeerae cateteeree aactaeteea acgaettgaa etecatggee ggetegeegg teteateeta etegteggae gagggetett aegaceeget eageeegag 1075 gagcaggagc ttctcgactt caccaactgg ttctgagggg ctcggcctgg tcaggccctg 1135 1195 gtgcgaatgg actttggaag cagggtgatc gcacaacctg catctttagt gctttcttgt 1255 gaagaagaaa aaaacgaaaa cagtcaacca accccatcgc caactaagcg aggcatgcct 1315 1375 gagagacatg gctttcagaa aacgggaagc gctcagaaca gtatctttgc actccaatca ttcacggaga tatgaagagc aactgggacc tgagtcaatg cgcaaaatgc agcttgtgtg 1435 1495 caaaagcagt gggctcctgg cagaagggag cagcacacgc gttatagtaa ctcccatcac ctctaacacg cacagetgaa agttettget egggteeett caceteeeeg ceetttetta 1555 1615 gagtgcagtt cttagccctc tagaaacgag ttggtgtctt tcgtctcagt agcccccacc 1675 ccaataagct gtagacattg gtttacagtg aaactatgct attctcagcc ctttgaaact ctgcttctcc tccagggccc gattcccaaa ccccatggct tccctcacac tgtcttttct 1735 1795 accattttca ttatagaatg cttccaatct tttgtgaatt ttttattata aaaaatctat ttgtatctat cctaaccagt tcggggatat attaagatat ttttgtacat aagagagaaa 1855 gagagagaaa aatttataga agttttgtac aaatggttta aaatgtgtat atcttgatac 1915 1975 tttaacatgt aatgctatta cctctgcata ttttagatgt gtagttcacc ttacaactgc 2035 aattttccct atgtggtttt gtaaagaact ctcctcatag gtgagatcaa gaggccacca 2095 gttgtacttc agcaccaatg tgtcttactt tatagaaatg ttgttaatgt attaatgatg ttattaaata ctgttcaaga agaacaaagt ttatgcagct actgtccaaa ctcaaagtgg 2155 2215 cagccagttg gttttgatag gttgcctttt ggagatttct attactgcct tttttttctt actgttttat tacaaactta caaaaatatg tataaccctg ttttatacaa actagtttcg 2275 2304 taataaaact ttttcctttt tttaaaatg

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Met Glu Ser Ser Ala Lys Met Glu Ser Gly Gly Ala Gly Gln Gln Pro 1 5 10 15

Gln Pro Gln Pro Gln Gln Pro Phe Leu Pro Pro Ala Ala Cys Phe Phe 20 25 30

Gln Leu Arg Pro Ala Ala Asp Gly Gln Pro Ser Gly Gly Gly His 65 70 75